

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/551,696
Source: PC7/p
Date Processed by STIC: 10/14/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 10/14/2005

PATENT APPLICATION: US/10/551,696

TIME: 13:28:39

Input Set : A:\seq list.txt

Output Set: N:\CRF4\10142005\J551696.raw

3 <110> APPLICANT: CropDesign N.V.
 4 Centre National de la Recherche Scientifique
 6 <120> TITLE OF INVENTION: Plants having improved growth characteristics and a method
 for making the
 7 same
 9 <130> FILE REFERENCE: BET 04P0246
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/551,696
 C--> 11 <141> CURRENT FILING DATE: 2005-09-30
 11 <150> PRIOR APPLICATION NUMBER: EP 03290812.1
 12 <151> PRIOR FILING DATE: 2003-03-31
 14 <160> NUMBER OF SEQ ID NOS: 19
 16 <170> SOFTWARE: PatentIn version 3.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1905
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Arabidopsis thaliana
 23 <220> FEATURE:
 24 <221> NAME/KEY: misc_feature
 25 <223> OTHER INFORMATION: CCS52A1 cDNA
 28 <400> SEQUENCE: 1
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 31 agaaacctat cgccggcgat gaatactccg gtggtttcac ttgagtcacg aatcaatcga 120
 33 ttaatcaatg ctaatcaatc tcaatcacca tcaccatcat cactatcaag gtctatatac 180
 35 tctgatagat ttatccccag tagatccgga tccaatttcg ctcttttcga tctatctcct 240
 37 tctcctagta aagatggtaa ggaagatgga gctggctctt acgctactct gttgcgtgcg 300
 39 gcgatgtttg gtctctgagac gccggagaag agagatatta ctgggttttc ttcttccagg 360
 41 aatattttta ggtttaagac ggagactcat cggctcttga attcgttttc tccttttggt 420
 43 gttgatgatg attctccttg tgtttctcat agtggctctg ttaaagctcc caggaaagtg 480
 45 ccgcgatcgc cgtataagat tcttgatctc gttgacttta gatctttggt ttcgataatg 540
 47 catgaaacaa tttgtgatct ttgtgatgtt ttggtctctg agggctctaga atttgagtct 600
 49 gaggtattgg atgcaccggc cttgcaagat gatttttata tgaatcttgt ggattggtct 660
 51 gcacaaaatg ttctagcagt gggactaggg aactgtgtgt atttatggaa tgctttagtc 720
 53 agcaagggtta ctaagttatg tgatctcgga gctgaggata gtgtttgctc agtgggttgg 780
 55 gcgttacgtg gaactcatct ggctgttgga actagtaccg ggaaagttca gatatgggat 840
 57 gcgtcacgct gcaagagaac aagaacaatg gaaggctcat gtctaagagt tggagccctg 900
 59 gcatgggggt catcgggtct gtcactctgg agcagagaca agagtattct tcagagagac 960
 61 ataagggtgtc aagaagatca tgtcagtaaa ttggcagggtc ataaatctga ggtatgcgga 1020
 63 ctcaagtggc cttatgacaa cagagagcta gcatctgggt gaaacgacaa taggcttttt 1080
 65 gtatggaacc aacattcaac acaaccgggt ttgaaatata gtgaacacac tgcagctggt 1140
 67 aaagccattg cttggtctcc tcatgttcat gggtctcttg cttctggtgg tggtagtct 1200
 69 gatagatgca tacgtttttg gaatacaacc acgaatactc atttaagttc catagatact 1260
 71 tgcagtcagg tatgcaatct agcttgggtc aagaacgtaa acgagcttgt tagcacacac 1320
 73 ggatactctc agaaccaaat cattgtctgg aaatacccaa ccatgtccaa aattgctact 1380
 75 ctaaccgggtc acacataacc agtcttatac cttgcgggtt caccgatgg acagacgatt 1440

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77 gtaacaggag caggagatga aaccttaagg ttctggaatg ttttcccttc cccaaaatct 1500
79 cagaacacgg atagtgaat cgggtcgtct ttctttggta gaacaacaat tcggtgagaa 1560
81 gttactttca aaacacacag aaaaagtcac aaattcttga tttcttcagc agcagccagc 1620
83 ttgagttggc cgtctcaacc aacttttttc acacgggagc agagagtcac taaattcttt 1680
85 tacacacgga tgcaacaaga tctaaccctt ttgatttaac cagcatcttt gggtttccat 1740
87 caagatgcac aacatttttc cccaaaattt tccaaagtgt atatctttat tcaatttttc 1800
89 ttcatatatc aaaatatagt ttcttttgta tttatttact tacgaacaca acattttata 1860
91 aaataagccc atgataataa tgcaataatt cgttaccatt ctctt 1905
94 <210> SEQ ID NO: 2
95 <211> LENGTH: 518
96 <212> TYPE: PRT
97 <213> ORGANISM: Arabidopsis thaliana
99 <220> FEATURE:
100 <221> NAME/KEY: MISC_FEATURE
101 <223> OTHER INFORMATION: CCS52A1 protein
104 <400> SEQUENCE: 2
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107 1 5 10 15
109 Ser Ser Ser Met Arg Asn Leu Ser Pro Ala Met Asn Thr Pro Val Val
110 20 25 30
112 Ser Leu Glu Ser Arg Ile Asn Arg Leu Ile Asn Ala Asn Gln Ser Gln
113 35 40 45
115 Ser Pro Ser Pro Ser Ser Leu Ser Arg Ser Ile Tyr Ser Asp Arg Phe
116 50 55 60
118 Ile Pro Ser Arg Ser Gly Ser Asn Phe Ala Leu Phe Asp Leu Ser Pro
119 65 70 75 80
121 Ser Pro Ser Lys Asp Gly Lys Glu Asp Gly Ala Gly Ser Tyr Ala Thr
122 85 90 95
124 Leu Leu Arg Ala Ala Met Phe Gly Pro Glu Thr Pro Glu Lys Arg Asp
125 100 105 110
127 Ile Thr Gly Phe Ser Ser Ser Arg Asn Ile Phe Arg Phe Lys Thr Glu
128 115 120 125
130 Thr His Arg Ser Leu Asn Ser Phe Ser Pro Phe Gly Val Asp Asp Asp
131 130 135 140
133 Ser Pro Gly Val Ser His Ser Gly Pro Val Lys Ala Pro Arg Lys Val
134 145 150 155 160
136 Pro Arg Ser Pro Tyr Lys Ile Leu Asp Leu Val Asp Phe Arg Ser Leu
137 165 170 175
139 Val Ser Ile Met His Glu Thr Ile Cys Asp Leu Cys Asp Val Leu Val
140 180 185 190
142 Ser Glu Gly Leu Glu Phe Glu Ser Glu Val Leu Asp Ala Pro Ala Leu
143 195 200 205
145 Gln Asp Asp Phe Tyr Leu Asn Leu Val Asp Trp Ser Ala Gln Asn Val
146 210 215 220
148 Leu Ala Val Gly Leu Gly Asn Cys Val Tyr Leu Trp Asn Ala Cys Ser
149 225 230 235 240
151 Ser Lys Val Thr Lys Leu Cys Asp Leu Gly Ala Glu Asp Ser Val Cys
152 245 250 255
154 Ser Val Gly Trp Ala Leu Arg Gly Thr His Leu Ala Val Gly Thr Ser

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157 Thr Gly Lys Val Gln Ile Trp Asp Ala Ser Arg Cys Lys Arg Thr Arg
158          275          280          285
160 Thr Met Glu Gly His Arg Leu Arg Val Gly Ala Leu Ala Trp Gly Ser
161          290          295          300
163 Ser Val Leu Ser Ser Gly Ser Arg Asp Lys Ser Ile Leu Gln Arg Asp
164 305          310          315          320
166 Ile Arg Cys Gln Glu Asp His Val Ser Lys Leu Ala Gly His Lys Ser
167          325          330          335
169 Glu Val Cys Gly Leu Lys Trp Ser Tyr Asp Asn Arg Glu Leu Ala Ser
170          340          345          350
172 Gly Gly Asn Asp Asn Arg Leu Phe Val Trp Asn Gln His Ser Thr Gln
173          355          360          365
175 Pro Val Leu Lys Tyr Ser Glu His Thr Ala Ala Val Lys Ala Ile Ala
176          370          375          380
178 Trp Ser Pro His Val His Gly Leu Leu Ala Ser Gly Gly Gly Thr Ala
179 385          390          395          400
181 Asp Arg Cys Ile Arg Phe Trp Asn Thr Thr Thr Asn Thr His Leu Ser
182          405          410          415
184 Ser Ile Asp Thr Cys Ser Gln Val Cys Asn Leu Ala Trp Ser Lys Asn
185          420          425          430
187 Val Asn Glu Leu Val Ser Thr His Gly Tyr Ser Gln Asn Gln Ile Ile
188          435          440          445
190 Val Trp Lys Tyr Pro Thr Met Ser Lys Ile Ala Thr Leu Thr Gly His
191          450          455          460
193 Thr Tyr Arg Val Leu Tyr Leu Ala Val Ser Pro Asp Gly Gln Thr Ile
194 465          470          475          480
196 Val Thr Gly Ala Gly Asp Glu Thr Leu Arg Phe Trp Asn Val Phe Pro
197          485          490          495
199 Ser Pro Lys Ser Gln Asn Thr Asp Ser Glu Ile Gly Ser Ser Phe Phe
200          500          505          510
202 Gly Arg Thr Thr Ile Arg
203          515
206 <210> SEQ ID NO: 3
207 <211> LENGTH: 2028
208 <212> TYPE: DNA
209 <213> ORGANISM: Oryza sativa
211 <220> FEATURE:
212 <221> NAME/KEY: misc_feature
213 <223> OTHER INFORMATION: CCS52A cDNA
216 <400> SEQUENCE: 3
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221 gtcgtcgcgcg ctcgcgcgcg cgccgtctct ccgcgtctcc tccgcggcgc cgcacccctc 180
223 ccgcgtctctc tccgcgcccc cgccggcctc gcggacgggtc tacagcgacc gcttcatccc 240
225 cagccgcgccc ggatccaacc tcgcgtcttt cgacctcgcc ccgtcgccgt cccaccaaga 300
227 cgccgcgcgcc gccgcgcgct ccccggcgc gccgcccccc tccggatcta ccccggcctc 360
229 gtcgcccctac tgcgcgtctc tccgcgcgc gctcttcggc cccaccacgc ccgaccgggt 420
231 ggcgtcgctcg gcgtccgcgt gctctctctc ctctccgcgc ggggcgtcgc ccgtgggctc 480

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233 acccgccacc ggcaacatat tcaggttcaa ggcggaggtg ccccggaatg ctaagcgcgc      540
235 ccttttctcc gacggggacg acgagggcgt gctcttcccc ggggtgttca cgacgagggg      600
237 cactggcccc aggaagatcc ctaggtcacc ttataaggtg ctggatgctc ccgcattgca      660
239 ggatgacttc tacctgaacc ttgtggattg gtcttcgcat aatatccttg cagttggatt      720
241 ggggaattgt gtctacttat ggaatgcatt cagcagcaag gtcaccaagc tatgtgattt      780
243 gggggtggat gacaatgtct gttcagtggt ttgggcacag cgtggcactc accttgctgt      840
245 agggacaaac caaggcaaag ttcaggtatg ggatgccact cgttgtaaga gaataagaac      900
247 catggaaagc catcggatgc gagtaggtgc tcttgcattg aattcatcat tgctttcgct      960
249 aggcagtcgt gacaagagca tccttcacca tgatatccgt gcccgaggtg attatattag     1020
251 tagacttgct gggcataaat cggaggtctg tgggctcaag tggctcttatg ataaccgtca     1080
253 gcttgcattc ggtggtaatg acaacagact ttatgtatgg aatcaacact cggcgacacc     1140
255 ggtactgaag tatactgagc atacagcagc tgtcaaagct attgcgtggt cacctcatct     1200
257 tcatgggctg cttgcatctg gtggaggaac tgcagataga tgcatacgat tttggaatac     1260
259 caccacgaat atgcacttaa attgcgtcga cacaggcagt caggtctgta atcttgatg     1320
261 gtcaaagaat gttaatgagc ttgttagcac tcatggatat tctcaaaatc agataattgt     1380
263 ttggcgatac ccaacaatgt caaagctcgc cacattgaca ggccatacat atagggtatt     1440
265 atatttagcc atctccccag atggacagac tatagtaact ggcgctggtg atgaaacgct     1500
267 tcggtttttg aacgtgtttc catctcccaa gtcccagagt tctgacagcc taagtagcat     1560
269 cggggccaca tcatttgtaa ggagctacat ccggtgacac tgagatgtgg taatctaata     1620
271 acacttggtc cataagtcac aacactactg cagcagagtg ttgatgatca tcaatatcat     1680
273 tccatttgta ccacttgcat caccagttca tgaaccatca aacctagcca aattttagag     1740
275 atagtaggat gcagaatggt gaaactggct cgcagacctc ggagtggctc atttgctgaa     1800
277 tgctgtatat atttattcat tggctttgta ggagcgaaga tggcaaacac tgaccatccg     1860
279 caatgtacca ttgataagtt cacggcctcc tgtttttggt tttgctgagt caacttggag     1920
281 ctggagctct tatgtatacc atgctagggc ttaacaacat tggccaactc atgatgctca     1980
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286 <210> SEQ ID NO: 4

287 <211> LENGTH: 507

288 <212> TYPE: PRT

289 <213> ORGANISM: Oryza sativa

291 <220> FEATURE:

292 <221> NAME/KEY: MISC_FEATURE

293 <223> OTHER INFORMATION: CCS52A protein

296 <400> SEQUENCE: 4

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302          20          25          30
304 Pro His Pro Ser Pro Ser Ser Ser Ala Pro Thr Pro Ala Ser Arg Thr
305          35          40          45
307 Val Tyr Ser Asp Arg Phe Ile Pro Ser Arg Ala Gly Ser Asn Leu Ala
308          50          55          60
310 Leu Phe Asp Leu Ala Pro Ser Pro Ser His His Asp Ala Ala Ala Ala
311 65          70          75          80
313 Ala Ala Ser Pro Gly Ala Pro Pro Pro Ser Gly Ser Thr Pro Ala Ser
314          85          90          95
316 Ser Pro Tyr Cys Ala Leu Leu Arg Ala Ala Leu Phe Gly Pro Thr Thr
317          100         105         110
319 Pro Asp Arg Val Ala Ser Ser Ala Ser Ala Cys Ser Ser Ser Ser Ser

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320          115          120          125
322 Ala Gly Ala Ser Pro Val Gly Ser Pro Ala Thr Gly Asn Ile Phe Arg
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325 Phe Lys Ala Glu Val Pro Arg Asn Ala Lys Arg Ala Leu Phe Ser Asp
326 145          150          155          160
328 Gly Asp Asp Glu Gly Val Leu Phe Pro Gly Val Phe Thr Thr Arg Gly
329          165          170          175
331 Thr Gly Pro Arg Lys Ile Pro Arg Ser Pro Tyr Lys Val Leu Asp Ala
332          180          185          190
334 Pro Ala Leu Gln Asp Asp Phe Tyr Leu Asn Leu Val Asp Trp Ser Ser
335          195          200          205
337 His Asn Ile Leu Ala Val Gly Leu Gly Asn Cys Val Tyr Leu Trp Asn
338          210          215          220
340 Ala Cys Ser Ser Lys Val Thr Lys Leu Cys Asp Leu Gly Val Asp Asp
341 225          230          235          240
343 Asn Val Cys Ser Val Gly Trp Ala Gln Arg Gly Thr His Leu Ala Val
344          245          250          255
346 Gly Thr Asn Gln Gly Lys Val Gln Val Trp Asp Ala Thr Arg Cys Lys
347          260          265          270
349 Arg Ile Arg Thr Met Glu Ser His Arg Met Arg Val Gly Ala Leu Ala
350          275          280          285
352 Trp Asn Ser Ser Leu Leu Ser Ser Gly Ser Arg Asp Lys Ser Ile Leu
353          290          295          300
355 His His Asp Ile Arg Ala Gln Asp Asp Tyr Ile Ser Arg Leu Ala Gly
356 305          310          315          320
358 His Lys Ser Glu Val Cys Gly Leu Lys Trp Ser Tyr Asp Asn Arg Gln
359          325          330          335
361 Leu Ala Ser Gly Gly Asn Asp Asn Arg Leu Tyr Val Trp Asn Gln His
362          340          345          350
364 Ser Ala His Pro Val Leu Lys Tyr Thr Glu His Thr Ala Ala Val Lys
365          355          360          365
367 Ala Ile Ala Trp Ser Pro His Leu His Gly Leu Leu Ala Ser Gly Gly
368          370          375          380
370 Gly Thr Ala Asp Arg Cys Ile Arg Phe Trp Asn Thr Thr Thr Asn Met
371 385          390          395          400
373 His Leu Asn Cys Val Asp Thr Gly Ser Gln Val Cys Asn Leu Val Trp
374          405          410          415
376 Ser Lys Asn Val Asn Glu Leu Val Ser Thr His Gly Tyr Ser Gln Asn
377          420          425          430
379 Gln Ile Ile Val Trp Arg Tyr Pro Thr Met Ser Lys Leu Ala Thr Leu
380          435          440          445
382 Thr Gly His Thr Tyr Arg Val Leu Tyr Leu Ala Ile Ser Pro Asp Gly
383          450          455          460
385 Gln Thr Ile Val Thr Gly Ala Gly Asp Glu Thr Leu Arg Phe Trp Asn
386 465          470          475          480
388 Val Phe Pro Ser Pro Lys Ser Gln Ser Ser Asp Ser Leu Ser Ser Ile
389          485          490          495
391 Gly Ala Thr Ser Phe Val Arg Ser Tyr Ile Arg
392          500          505

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; Xaa Pos. 1,3,4,5,6
Seq#:8; Xaa Pos. 1,2,3,4,5,6,8,9,12,13,14,15
Seq#:9; Xaa Pos. 1,2,3,4,6,7,11,12,13,14,17,18
Seq#:11; Xaa Pos. 2,3,5,7
Seq#:12; Xaa Pos. 3,4,6,8,9,10
Seq#:13; Xaa Pos. 5,6,7,8,10,11,12
Seq#:14; Xaa Pos. 5
Seq#:15; Xaa Pos. 1,2,4,5,6,7,8,9,10,11
Seq#:16; Xaa Pos. 6
Seq#:17; Xaa Pos. 4,9

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:809 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0